



Release 3.1a John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat May 13 10:22:35 2000; MasPar time 3.95 Seconds
Tabular output not generated. 258.173 Million cell updates/sec

Title: >US-09-331-631-5
Description: (33-75) from US09331631.pep (2 of 4)
Perfect Score: 343
Sequence: 1 NOEDPOTECOCORRCROESDPDPOOYCORCKEICEEBEY 43

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseqs5
1:geneseqp

Statistics: Mean 22.157; Variance 99.354; scale 0.223

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	343	100.0	625	1	Macadamia integrifolia	1.45e-22
2	337	98.3	666	1	Macadamia integrifolia	5.15e-22
3	335	97.7	666	1	Macadamia integrifolia	7.86e-22
4	155	45.2	525	1	Theobroma cacao anti	1.09e-05
5	155	45.2	566	1	Sequence encoded by 67	1.09e-05
6	135	39.4	590	1	Gossypium hirsutum ant	5.57e-04
7	119	34.7	28	1	Stenocarpus sinuatus a	1.22e-02
8	115	33.5	593	1	Zea mays antimicrobial	8.17e-02
9	109	31.8	33	1	Antimicrobial maize pe	4.40e-01
10	100	29.2	35	1	Antimicrobial maize pe	3.96e+00
11	88	25.7	626	1	Peanut allergen Ara hi	6.80e+00
12	85	24.6	637	1	Hordeum vulgare anti	9.73e+00
13	83	24.2	106	1	AcanaP24.	9.73e+00
14	83	24.2	107	1	AcanaP23.	9.73e+00
15	83	24.2	441	1	Steroid hormone recept	9.73e+00
16	83	24.2	441	1	Peroxisome proliferato	9.73e+00
17	83	24.2	614	1	Arachis hypogaea antim	9.73e+00
18	83	24.2	614	1	Peanut allergen Ara hi	9.73e+00
19	79	23.0	439	1	XR4.	1.98e+01
20	79	23.0	440	1	Mouse peroxisome proli	1.98e+01
21	79	23.0	440	1	Peroxisome proliferato	1.98e+01
22	79	23.0	919	1	Human androgen recepto	1.98e+01
23	79	23.0	919	1	Androgen receptor.	1.98e+01

ID	Score	Query Match	Length	ID	Description	Pred. No.
24	76	22.2	516	1	Soybean glycinin A3B4	3.35e+01
25	76	22.2	918	1	Human androgen recepto	3.98e+01
26	75	21.9	204	1	DNA-binding/dimerizati	3.98e+01
27	75	21.9	468	1	Human peroxisome proli	3.98e+01
28	75	21.9	768	1	Rabbit beta-8 intergri	3.98e+01
29	74	21.6	55	1	Murine vascular endothe	4.74e+01
30	74	21.6	55	1	Vascular endothelial g	4.74e+01
31	74	21.6	145	1	Human VEGF-B truncated	4.74e+01
32	74	21.6	147	1	Human VEGF-B truncated	4.74e+01
33	74	21.6	150	1	Human VEGF-B truncated	4.74e+01
34	74	21.6	152	1	Human VEGF-B truncated	4.74e+01
35	74	21.6	155	1	Human VEGF-B truncated	4.74e+01
36	74	21.6	160	1	Human VEGF-B truncated	4.74e+01
37	74	21.6	167	1	Human VEGF-B full leng	4.74e+01
38	74	21.6	188	1	Human vascular endothe	4.74e+01
39	74	21.6	188	1	Heart vascular endothe	4.74e+01
40	74	21.6	188	1	Murine vascular endothe	4.74e+01
41	74	21.6	190	1	AcenaP4.	4.74e+01
42	74	21.6	195	1	Murine vascular endothe	4.74e+01
43	74	21.6	195	1	Human vascular endothe	4.74e+01
44	74	21.6	176	1	Human laminin BI chain	4.74e+01
45	73	21.3	188	1	Murine VWF167.	5.63e+01

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description	Pred. No.
1	W62830	100.0%	Score 343; DB 1; Length 625; Best local Similarity 100.0%; Pred. No. 1.45e-22; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	625	1	Macadamia integrifolia	1.45e-22
2	W62830	98.3%	Score 337; DB 1; Length 666; Best local Similarity 98.3%; Pred. No. 5.15e-22; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	666	1	Macadamia integrifolia	5.15e-22
3	W62830	97.7%	Score 335; DB 1; Length 666; Best local Similarity 97.7%; Pred. No. 7.86e-22; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	666	1	Macadamia integrifolia	7.86e-22
4	W62831	45.2%	Score 155; DB 1; Length 525; Best local Similarity 45.2%; Pred. No. 1.09e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	525	1	Theobroma cacao anti	1.09e-05
5	W62831	45.2%	Score 155; DB 1; Length 566; Best local Similarity 45.2%; Pred. No. 1.09e-05; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	566	1	Sequence encoded by 67	1.09e-05
6	W62832	39.4%	Score 135; DB 1; Length 590; Best local Similarity 39.4%; Pred. No. 5.57e-04; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	590	1	Gossypium hirsutum ant	5.57e-04
7	W62841	34.7%	Score 119; DB 1; Length 28; Best local Similarity 34.7%; Pred. No. 1.22e-02; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	28	1	Stenocarpus sinuatus a	1.22e-02
8	W62835	33.5%	Score 115; DB 1; Length 593; Best local Similarity 33.5%; Pred. No. 8.17e-02; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	593	1	Zea mays antimicrobial	8.17e-02
9	W62836	31.8%	Score 109; DB 1; Length 33; Best local Similarity 31.8%; Pred. No. 4.40e-01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	33	1	Antimicrobial maize pe	4.40e-01
10	W62837	29.2%	Score 100; DB 1; Length 35; Best local Similarity 29.2%; Pred. No. 3.96e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	35	1	Antimicrobial maize pe	3.96e+00
11	W62837	25.7%	Score 88; DB 1; Length 626; Best local Similarity 25.7%; Pred. No. 6.80e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	626	1	Peanut allergen Ara hi	6.80e+00
12	W62837	24.6%	Score 85; DB 1; Length 637; Best local Similarity 24.6%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	637	1	Hordeum vulgare anti	9.73e+00
13	W62837	24.2%	Score 83; DB 1; Length 106; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	106	1	AcanaP24.	9.73e+00
14	W62837	24.2%	Score 83; DB 1; Length 107; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	107	1	AcanaP23.	9.73e+00
15	W62837	24.2%	Score 83; DB 1; Length 441; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	441	1	Steroid hormone recept	9.73e+00
16	W62837	24.2%	Score 83; DB 1; Length 441; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	441	1	Peroxisome proliferato	9.73e+00
17	W62837	24.2%	Score 83; DB 1; Length 614; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	614	1	Arachis hypogaea antim	9.73e+00
18	W62837	24.2%	Score 83; DB 1; Length 614; Best local Similarity 24.2%; Pred. No. 9.73e+00; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	614	1	Peanut allergen Ara hi	9.73e+00
19	W62837	23.0%	Score 79; DB 1; Length 439; Best local Similarity 23.0%; Pred. No. 1.98e+01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	439	1	XR4.	1.98e+01
20	W62837	23.0%	Score 79; DB 1; Length 440; Best local Similarity 23.0%; Pred. No. 1.98e+01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	440	1	Mouse peroxisome proli	1.98e+01
21	W62837	23.0%	Score 79; DB 1; Length 440; Best local Similarity 23.0%; Pred. No. 1.98e+01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	440	1	Peroxisome proliferato	1.98e+01
22	W62837	23.0%	Score 79; DB 1; Length 919; Best local Similarity 23.0%; Pred. No. 1.98e+01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	919	1	Human androgen recepto	1.98e+01
23	W62837	23.0%	Score 79; DB 1; Length 919; Best local Similarity 23.0%; Pred. No. 1.98e+01; Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	919	1	Androgen receptor.	1.98e+01

FT Protein 29. .666
 /note="mature protein"
 PN M09827805-A1.
 PD 02-JUL-1998.
 PE 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 NR N-PSDB: V42310.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 34-36; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 be used to control microbial infestations in plants and mammalian
 CC animals.
 CC
 SO Sequence 666 AA;

Query Match 98.3%; Score 337; DB 1; Length 666;
 Best Local Similarity 97.7%; Pred. No. 5.15e-22;
 Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 74 NOEDPOTECQCCQRCRQESGPRROOYQCRCKEICEEERY 116
 QY 33 NOEDPOTECQCCQRCRQESDPROOYQCRCKEICEEERY 75

RESULT 3
 ID M62829 standard; Protein; 666 AA.
 AC M62829.
 DT 27-OCT-1998 (first entry)
 DE Macadamia integrifolia antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Macadamia integrifolia.
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT Protein /note="signal peptide"
 FT Protein /note="mature protein"

PN M09827805-A1.
 PD 02-JUL-1998.
 PE 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 NR N-PSDB: V42311.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 39-41; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 be used to control microbial infestations in plants and mammalian
 CC animals.
 CC
 SO Sequence 666 AA;

Query Match 97.7%; Score 335; DB 1; Length 666;
 Best Local Similarity 93.0%; Pred. No. 7.86e-22;
 Matches 40; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 74 NOEDPOTECQCCQRCRQESGPRROOYQCRCKEICEEERY 116
 QY 33 NOEDPOTECQCCQRCRQESDPROOYQCRCKEICEEERY 75

RESULT 4
 ID M62831 standard; Protein; 525 AA.
 AC M62831.
 DT 27-OCT-1998 (first entry)
 DE Theobroma cacao antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Theobroma cacao.
 PN M09827805-A1.
 PD 02-JUL-1998.

PF 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 NR N-PSDB: V42310.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 47-49; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 be used to control microbial infestations in plants and mammalian
 CC animals.
 CC
 SO Sequence 525 AA;

Query Match 45.2%; Score 155; DB 1; Length 525;
 Best Local Similarity 47.5%; Pred. No. 1.09e-05;
 Matches 19; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

DB 78 EEEIQRQYQCCQRCRQESGPRROOYQCRCKEICEEERY 117
 QY 34 QEDPOTECQCCQRCRQESDPROOYQCRCKEICEEERY 73

RESULT 5
 ID R20181 standard; Protein; 566 AA.
 AC R20181.
 DT 16-APR-1992 (first entry)
 DE Sequence encoded by 67 kD T. cacao protein cDNA.
 KW Cocoa; flavour; vicillin; seed storage protein.
 OS Theobroma cacao.
 PN M09119801-A.
 PD 26-DEC-1991.
 PE 07-JUN-1991; G00914.
 PR 11-JUN-1990; GB-013016.
 PA (MRSC) MARS UK LTD.
 PI Spencer ME, Hodge R, Deakin EA, Ashton S;
 DR WPI: 92-024418/03.
 NR N-PSDB: Q20377.
 PT Recombinant cocoa proteins - are responsible for flavour in cocoa
 PT beans and produced in large quantities using yeast and bacterial
 PT expression vectors
 PS Claim 4; Fig 2; 59pp; English.
 CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
 CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
 CC derived from the 67 kD precursor. T. cacao protein cDNA was
 CC detected in a cDNA library prepared from immature cocoa beans RNA
 CC using a probe based on the AA sequence of a CNBR peptide common to
 CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
 CC homologues between the 67 kD polypeptide and the vicillins, which are
 CC seed storage proteins.
 CC
 SO Sequence 566 AA;

Query Match 45.2%; Score 155; DB 1; Length 566;
 Best Local Similarity 47.5%; Pred. No. 1.09e-05;
 Matches 19; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

DB 78 EEEIQRQYQCCQRCRQESGPRROOYQCRCKEICEEERY 117
 QY 34 QEDPOTECQCCQRCRQESDPROOYQCRCKEICEEERY 73

RESULT 6
 ID M62832 standard; Protein; 590 AA.
 AC M62832.
 DT 27-OCT-1998 (first entry)
 DE Gossypium hirsutum antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Gossypium hirsutum.
 PN M09827805-A1.
 PD 02-JUL-1998.
 PE 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;

